IN THE SPECIFICATION:

Page 12, beginning at line 22, please insert the following paragraph after the title to read as follows:

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

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Page 13, beginning at line 10, please amend the paragraph to read as follows:

FIGURE 2 Provides synthetic oligopeptides prepared for IL-16 inhibition experiments. Among other D4 sequences, the ~~three~~ two 12-residue peptides designated A~~,~~ and B~~, and C~~ and the 6-residue peptide designated C were uniquely found to inhibit IL-16 (below). The residues within peptide A and peptide B required for IL-16 inhibition were tested by using the 6-residue peptides shown. These include native sequences and peptides with non-conservative amino acid substitutions.

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Page 13, beginning at line 19, please amend the paragraph to read as follows:

FIGURE 3 Demonstrates IL-16 inhibition by 12-residue domain 4 peptides. The 12-residue peptides A, B, and C were tested for their capacity to inhibit murine IL-16 induced murine splenocyte chemotaxis. Serial $\log_{10}$ dilutions of each peptide from 10^{-9} ~~$^{-5}$~~ M to 10^{-5} ~~$^{-9}$~~ M, or control buffer without peptides, were combined with rIL-16 (10^{-9} M) and applied to the lower wells of Boyden microchemotaxis chambers. Peptide D is a random 12-residue oligopeptide used as a negative control. Cell migration was compared with migration in control buffer without IL-16 or peptides. Results are expressed as the mean % unstimulated control migration $\pm$ SEM for five experiments. Asterisks indicate a significant difference ($p < 0.05$) in migration

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between cells stimulated with rIL-16 alone and cells stimulated with rIL-16 in the presence of peptide.

Page 19, beginning at line 7, please amend the paragraph to read as follows:

By "IL-16 antagonist peptide" is meant a peptide that inhibits, suppresses or causes the cessation of at least one IL-16-mediated biological activity by e.g., binding to IL-16, interfering with, or preventing the binding of IL-16 to the CD4 receptor. An IL-16 antagonist functions in two ways. The antagonist can bind to or sequester IL-16 with sufficient affinity and specificity to substantially interfere with, block or otherwise prevent binding of IL-16 to an IL-16 receptor, thereby inhibiting, suppressing or causing the cessation of at least one IL-16-mediated biological activity, such as T-cells chemotaxis, for example. This type of IL-16 antagonist, also termed a "sequestering antagonist" is a specific feature of this invention. Alternatively, an IL-16 antagonist can compete with IL-16 for the cell surface receptor thereby interfering with, blocking or otherwise preventing the binding of IL-16 to an IL-16 receptor. This type of antagonist, e.g., which binds the receptor but does not trigger signal transduction, is also referred to herein as a "competitive antagonist". The contemplated "competitive antagonists" are, more specifically, described in commonly owned co-pending application Serial No. 09/368,632, filed on August 5, 1999, entitled "IL-16 Antagonists" (Docket No. 12875), the disclosure of which is incorporated herein by reference. The peptide antagonists are useful in the therapy of immunoinflammatory responses. Additionally, analogs, homologs and fragments of the novel peptides provided herein are included within the scope of the term "IL-16 antagonist peptide".

Page 40, beginning at line 3, please amend the paragraph to read as follows:

Cell migration was assessed using a modified Boyden chamber. (Center, et al., (1982) *J. Immunol.* 128:2563-2568; Cruikshank, et al., (1982) *J. Immunol.* 128:2569-2574). Murine splenocytes (5 x 10^6 cells/ml) in M199-HPS (or M199-HPS alone) was added to the bottom wells. For blocking experiments, 10^{-9} M murine rIL-16 with various concentrations of oligopeptides were mixed and placed in the lower well. The upper and lower wells were separated by 8 ~~u~~μm pore size nitrocellulose filter membrane (Neuro Probe). Following incubation (3 h, 37°C), the membranes were removed, stained with hematoxylin, and dehydrated. Cell migration was quantified by counting the number of cells migrating beyond a depth of 40 ~~u~~μm. Counts were compared with control cells exposed to M199-HPS alone, which was normalized to 100%. Cell migration is expressed as the mean % control migration. All samples were tested in duplicate, with five high power fields counted in each duplicate.

Page 42, beginning at line 29, please amend the paragraph to read as follows:

Murine spleens were harvested from healthy 8-week male BALB/c mice (Jackson Laboratory). Splenocytes were isolated by grinding spleens between frosted slides in M199 culture medium (M.A. Bioproducts), supplemented with 0.4% bovine serum albumin, 22 mM HEPES buffer, 100 with U/ml of penicillin, 100 ~~u~~μg/ml streptomycin (M199-HPS). Cells were washed and erythrocytes were lysed in Gey's solution. Splenocytes were washed twice in M199, and resuspended to a final concentration of 2 x 10^6 cells/ml in RPMI1640 medium (BioWhittaker) supplemented with 10% FBS, 100 U/ml of penicillin and 100 ~~u~~μg/ml of streptomycin. By flow cytometry, 25% of the isolated splenocytes within the lymphocyte-cloud were $CD4^+$.

Page 49, beginning at line 19, please amend the paragraph to read as follows:

To investigate IL-16 interaction with the D3D4 of CD4, the GST-D3D4 fusion protein, or GST alone, was bound to the glutathione-conjugated Sepharose 4B beads. Five ~~u~~µl of the *in vitro* translation product containing ^{35}S-labeled rIL16 was added to 15 ~~u~~µl of the bead-bound proteins in 230 ~~u~~µl of PBS and 50 ~~u~~µl of NETN buffer (150 mM NaC1, 1 mM EDTA, 0.5% NP 40, and 50 mM Tris, pH 8.0). After incubating at 4°C for 2 h, the beads were washed 3 times in NETN buffer. The GST-D3D4 or GST proteins were released from the beads by boiling in SDS gel loading buffer, and the supernatant was analyzed by 12% SDS-polyacrylamide gel electrophoresis (SDS-PAGE). The presence of ^{35}S-labeled mrIL16 was detected by autoradiography of the dried gel. Specificity was demonstrated by competition with an excess (10^{-5} M) of unlabeled rIL-16, and the effects of the three 12-residue D3D4 domain peptides on rIL-16 binding was tested by adding each peptide (10^{-5} M) to the binding reaction at time zero.

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Page 55, beginning at line 25, please amend the paragraph to read as follows:

Cell migration was assessed using a modified Boyden chamber. (Center, et al., (1982) *J. Immunol.* 128:2563-2568; Cruikshank, et al., (1982) *J. Immunol.* 128:2569-2574). Murine T-lymphocytes (5 x 10^6 cells/ml) in M199-HPS were loaded into the top wells of a microchemotaxis chamber, with 10^{-9} M murine rIL-16 in M199-HPS (or M199-HPS alone) was added to the bottom wells. For blocking experiments, 10^{-9} M murine rIL-16 with various concentrations of oligopeptides were mixed and placed in the lower well. The upper and lower wells were separated by 8 ~~u~~µm pore size nitrocellulose filter membrane (Neuro Probe). Following incubation (3 h, 37°C), the membranes were removed, stained with hematoxylin, and dehydrated. Cell migration was quantified by counting the number of cells migrating beyond a

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depth of 40 ~~u~~μm. Counts were compared with control cells exposed to M199-HPS alone, which was normalized to 100%. Cell migration is expressed as the mean % control migration. All samples were tested in duplicate, with five high power fields counted in each duplicate.

Page 58, beginning at line 3, please amend the paragraph to read as follows:

To confirm that the D4 domain was essential for an IL-16/CD4 interaction, peptides based on the amino acid sequence of the human CD4 D4 domain were generated. A 16 amino acid sequence encompassing the proximal portion of the D4 domain (GMWQCLLSDSGQVLLE, SEQ ID NO:12) blocked all IL-16-induced migration of human T-cells at a concentration of 10^{-10} M in the assay described in Example 1. In contrast, 16-mer peptides TSPKLMLSLKLENKEA (SEQ ID NO:38) and KVSKREKAVWVLNPEA (SEQ ID NO:39) failed to effect IL-16-induced migration at any concentration. A dose curve of the peptide indicated that maximal inhibition was achieved at a concentration of 10~~u~~μg/ml and greater. (Fig. 12).

To further identify the core active sequence within human CD4, two 8-residue peptides were generated. DSGQVLLE (amino acids 351:358; (SEQ ID NO:40) failed to inhibit IL-16-mediated biological activity. However, peptide GMWQCLLS (amino acids 343-350 (SEQ ID NO:13) inhibited all IL-16-mediated biological activity. The active site was further delineated by the use of tetrapeptides GMWQ (SEQ ID NO:41) and CLLS (SEQ ID NO:2). As shown in Figure 13 co-incubation of IL-16 and CLLS blocked approximately 90% of IL-16-induced migration of human T-cells. The inhibitory activity of CLLS on IL-16 bioactivity was not as a result of disruption of normal CD4 activity, as co-incubation with two other CD4 ligands capable of inducing migration, HIV-1 gp120 (5~~u~~μg/ml) and anti-CD4 antibody (OKT4, 1~~u~~μg/ml), were

unaffected. Gp120 binds to CD4 in the D1D2 region while the OKT4 antibody has been mapped to associate with CD4 in the D3 region. (Fig. 14).

Please amend the abstract to read as follows:

In accordance with the present invention, novel IL-16 antagonists, preferably peptides derived from CD4, have been isolated and synthesized. These peptides possess IL-16 antagonistic properties including the ability to selectively bind to IL-16 and inhibit IL-16-mediated biological activity. The peptides comprise specific portions of the native human CD4 receptor and variations thereof and therefore are non-immunogenic when administered to humans. The present invention also provides compositions containing at least one IL-16 antagonist peptide which can inhibit, suppress or cause the cessation of at least one IL-16-mediated biological activity in mammals, including humans. The present invention provides a method and composition for treating inflammation associated with disease states such as asthma, rheumatoid arthritis, inflammatory bowel disease (IBD) and systemic lupus (SLE) in mammals such as, for example, humans.